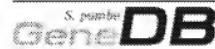


# CDS: isp6



WARNING: 30th July 2008

We continue to have problems downloading Boolean search results. We are working to resolve them.

Search for	Go To	Organisms	▼	Go To	Shortcuts	▼	Contact curator
------------	-------	-----------	---	-------	-----------	---	-----------------

## General Information

Name	isp6
Systematic Name	SPAC4A8.04
Gene Synonyms	prb1
Status	experimentally characterised (or published)
Product	vacuolar serine protease Isp6
Type	CDS
Sequence	DNA and Protein

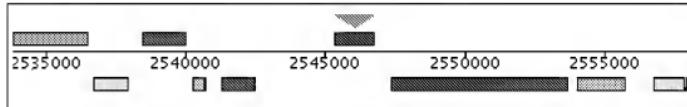
## Location

Chromosome	1
Contig Location	2545350..2546753 (Unspliced length: 1404 bp)
Exons	2545350..2546753 (Spliced length: 1404 bp)

[Region download  
and display \(in  
Artemis\)](#)

[Genome Browser](#)

## Context Map:



SPAC25H1.07 SPAC25H1.08c mdc5 SPAC4A8.02c ptc4 >isp6< myp2 SPAC4A8.06c SPAC4A8.07c

## Curation

Term	Db xref/URL	Other genes annotated to this term
expressed during nitrogen starvation	PMID:11872168	(2 Others)
conserved eukaryotic family		(866 Others)
similar to S. cerevisiae YEL060C		(1 Other)
similar to S. pombe SPAC1006.01		(0 Others)

## Predicted Peptide Properties

Mass	49.3 kDa	Amino acids	467
Isoelectric point	pH 5.2	Charge	-12.0

Signal peptide predicted for SPAC4A8.04 by SignalP 2.0 HMM (Signal peptide probability 0.999, signal anchor probability 0.000) with cleavage site probability 0.874 between residues 24 and 25

Transmembrane Domains	0 found
GPI Anchor	GPI-Anchor Signal predicted for SPAC4A8.04 by DGPI v2.04 with cleavage site probability 1.5480001 near 430

### Gene Ontology Annotation

Term (browse Amigo)	Qualifier Evidence	Other genes annotated to this term
<b>Biological Process</b>		
<u>RNA catabolic process</u>	IGI (PMID:11872168) with pnu1	<u>75 others</u>
<u>autophagy</u>	IMP (PMID:16550352)	<u>24 others</u>
<u>cellular response to nitrogen starvation</u>	IEP (PMID:11872168)	<u>30 others</u>
<u>cellular response to nitrogen starvation</u>	IMP (PMID:16550352)	<u>30 others</u>
<u>conjugation with cellular fusion</u>	IMP (PMID:7954893)	<u>103 others</u>
<u>proteolysis involved in cellular protein catabolic process</u>	IMP (PMID:11872168)	<u>167 others</u>
<u>regulation of nitrogen compound metabolic process</u>	IMP (PMID:16550352)	<u>5 others</u>
<u>vacuole organization and biogenesis</u>	IMP (PMID:16550352)	<u>44 others</u>
<b>Cellular Component</b>		
<u>Golgi apparatus</u>	IDA (PMID:16823372)	<u>356 others</u>
<u>vacuole</u>	TAS (PMID:16550352)	<u>145 others</u>
<b>Molecular Function</b>		
<u>serine-type endopeptidase activity</u>	IEA (GOA:spkwlGO_REF:0000004) with SP_KW:KW-0720	<u>13 others</u>
<u>serine-type peptidase activity</u>	ISS (PMID:17072883) with Pfam:PF00082	<u>18 others</u>

### Catalytic Activity

EC 3.4.21.- : IUBMB

EC 3.4.24.- : IUBMB

### Published Expression Profiles

Gene Expression Viewer Cell Cycle Meiosis Environmental Stress Pheromone Response/Mating

TranscriptomeViewer SPAC4A8.04 High-resolution view of transcripts in neighbourhood

### Literature

Search for isp6 in PubMed

### Domain Information

View Pfam domain structure for this gene product

View SCOP superfamily

DB	Accs	Description
Pfam	PF05922	Subtilisin N-terminal Region
Pfam	PF00082	Subtilase family
MEROPS	S08.052	MEROPS
InterPro	IPR000209	Peptidase S8 and S53, subtilisin, kexin, sedolisin
InterPro	IPR010259	Proteinase inhibitor I9, subtilisin propeptide
InterPro	IPR015500	Subtilisin-related serine protease

PRINTS	PR00723	Subtilisin serine protease family (S8) signature
PROSITE	PS00136	Serine proteases, subtilase family, aspartic acid active site.
PROSITE	PS00137	Serine proteases, subtilase family, histidine active site.
PROSITE	PS00138	Serine proteases, subtilase family, serine active site.

---

#### Database Cross-References

DB	Accs	Description
UniProtKB	P40903	Sexual differentiation process putative subtilase-type proteinase isp6 (EC 3.4.21.-).
EMBL	D14063	Schizosaccharomyces pombe mRNA for serine protease, complete cds.
EMBL	CU329670	Schizosaccharomyces pombe chromosome I
Biotwiki	SPAC4A8_04	Biotwiki
NCBI Entrez Gene	SPAC4A8.04	NCBI Entrez Gene
FYSSION	SPAC4A8.04	FYSSION
GermOnline	SPAC4A8.04	GermOnline
NBRP	SPAC4A8.04	Fission yeast strain database, National BioResource Project (Japan)
PIR	S45493	PIR
YOGY	SPAC4A8.04	Retrieval of eukaryotic orthologs

---

#### UniProtKB Annotation For This Protein

Developmental Stage	Transcribed specifically during sexual development.
Similarity	Belongs to the peptidase S8 family.
Keywords	Complete proteome (4982 others), Hydrolase (451 others), Protease (90 others), Serine protease (8 others)

This UniprotKB entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

---

Hosted by the [Sanger Institute](#)

[Curator feedback](#)

[Technical feedback](#)